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9

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/673,166
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 _____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

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1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/673,166

DATE: 08/19/2002

TIME: 12:54:26

Input Set : A:\102.174.txt

Output Set: N:\CRF3\08192002\I673166.raw

3 <110> APPLICANT: Le Gal, Frederique Anne
 4 Guillet, Jean Gerard
 5 Gahery-Segard, Hanne
 6 Gras-Masse, Helene
 7 Melnyk, Oleg
 8 Tartar, Andre
 10 <120> TITLE OF INVENTION: LIPOPEPTIDES INDUCING T LYMPHOCYTIC CYTOTOXICITY
 11 BEARING AT LEAST ONE AUXILIARY T EPITOPE, AND USES FOR
 12 VACCINATION

14 <130> FILE REFERENCE: 102.174
 16 <140> CURRENT APPLICATION NUMBER: 09/673,166
 17 <141> CURRENT FILING DATE: 2001-04-04
 19 <150> PRIOR APPLICATION NUMBER: PCT/FR99/00792
 20 <151> PRIOR FILING DATE: 1999-04-06

22 <160> NUMBER OF SEQ ID NOS: 276
 24 <170> SOFTWARE: PatentIn Ver. 2.1

26 <210> SEQ ID NO: 1

27 <211> LENGTH: 14

28 <212> TYPE: PRT

29 <213> ORGANISM: Clostridium tetanus

31 <220> FEATURE:

32 <223> OTHER INFORMATION: amino acids 830-843 of the tetanus toxin

34 <400> SEQUENCE: 1

35 Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu

36 1 5 10

39 <210> SEQ ID NO: 2

40 <211> LENGTH: 14

41 <212> TYPE: PRT

42 <213> ORGANISM: Human Papillomavirus (HPV)

44 <220> FEATURE:

45 <223> OTHER INFORMATION: amino acids 43-57 of HPV E7 protein

47 <400> SEQUENCE: 2

48 Gly Gln Ala Glu Pro Asp Arg Ala His Asn Ile Val Thr Phe

49 1 5 10

52 <210> SEQ ID NO: 3

53 <211> LENGTH: 28

54 <212> TYPE: PRT

55 <213> ORGANISM: Artificial Sequence

57 <220> FEATURE:

58 <221> NAME/KEY: LIPID

59 <222> LOCATION: (1)

60 <223> OTHER INFORMATION: dipalmitoyl-lysyl chain on N-terminal residue

62 <400> SEQUENCE: 3

Does Not Comply
 Corrected Diskette Needed

pp 1-3

(see item 11 on Encl
 Summary Sheet)

The source of genetic material
 for the entire
 Artificial
 Sequence needs
 to be
 explained. 8/19/02

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63 Ser Ser Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu
64 1 5 10 15
66 Ala Ala Ala Ala Ala Gly Ile Gly Ile Leu Thr Val
67 20 25

70 <210> SEQ ID NO: 4

71 <211> LENGTH: 28

72 <212> TYPE: PRT

73 <213> ORGANISM: Artificial Sequence

75 <220> FEATURE:

76 <221> NAME/KEY: LIPID

77 <222> LOCATION: (1)

78 <223> OTHER INFORMATION: dipalmitoyl-lysyl chain on N-terminal residue

80 <400> SEQUENCE: 4

81 Ser Ser Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu

82 1 5 10 15

84 Arg Gly Arg Ala Ala Gly Ile Gly Ile Leu Thr Val

85 20 25

88 <210> SEQ ID NO: 5

89 <211> LENGTH: 28

90 <212> TYPE: PRT

91 <213> ORGANISM: Artificial Sequence

93 <220> FEATURE:

94 <221> NAME/KEY: LIPID

95 <222> LOCATION: (1)

96 <223> OTHER INFORMATION: dipalmitoyl-lysyl chain on N-terminal residue

98 <400> SEQUENCE: 5

99 Gly Arg Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu

100 1 5 10 15

102 Arg Gly Arg Ala Ala Gly Ile Gly Ile Leu Thr Val

103 20 25

106 <210> SEQ ID NO: 6

107 <211> LENGTH: 28

108 <212> TYPE: PRT

109 <213> ORGANISM: Artificial Sequence

111 <220> FEATURE:

112 <221> NAME/KEY: LIPID

113 <222> LOCATION: (1)

114 <223> OTHER INFORMATION: monopalmitoyl-lysyl chain on N-terminal residue

116 <400> SEQUENCE: 6

117 Ser Ser Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu

118 1 5 10 15

120 Arg Gly Arg Ala Ala Gly Ile Gly Ile Leu Thr Val

121 20 25

124 <210> SEQ ID NO: 7

125 <211> LENGTH: 28

126 <212> TYPE: PRT

127 <213> ORGANISM: Artificial Sequence

129 <220> FEATURE:

130 <221> NAME/KEY: LIPID

entire sequence needs to be explained

same error

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131 <222> LOCATION: (1)
 132 <223> OTHER INFORMATION: monopalmitoyl-lysyl chain on N-terminal residue
 134 <400> SEQUENCE: 7
 135 Gly Arg Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu
 136 1 5 10 15
 138 Arg Gly Arg Ala Ala Gly Ile Gly Ile Leu Thr Val
 139 20 25
 142 <210> SEQ ID NO: 8
 143 <211> LENGTH: 10
 144 <212> TYPE: PRT
 145 <213> ORGANISM: Artificial Sequence
 147 <220> FEATURE:
 148 <223> OTHER INFORMATION: A hydrazine is bound between the N-terminal lysine
 149 and isoleucine at position 2
 151 <400> SEQUENCE: 8
 152 Lys Ile Leu Lys Glu Pro Val His Gly Val
 153 1 5 10
 156 <210> SEQ ID NO: 9
 157 <211> LENGTH: 15
 158 <212> TYPE: PRT
 159 <213> ORGANISM: Artificial Sequence
 161 <220> FEATURE:
 162 <223> OTHER INFORMATION: aldehyde group bound to N- terminal residue
 164 <220> FEATURE:
 165 <221> NAME/KEY: LIPID
 166 <222> LOCATION: (15)
 167 <223> OTHER INFORMATION: palmitoyl chain on C-terminal lysine residue
 169 <400> SEQUENCE: 9
 170 Arg Thr Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Lys
 171 1 5 10 15
 174 <210> SEQ ID NO: 10
 175 <211> LENGTH: 9
 176 <212> TYPE: PRT
 177 <213> ORGANISM: Homo sapiens
 179 <220> FEATURE:
 180 <223> OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic
 181 myeloid leukemia translocation)
 183 <400> SEQUENCE: 10
 184 Glu Asp Ala Glu Leu Asn Pro Arg Phe
 185 1 5
 188 <210> SEQ ID NO: 11
 189 <211> LENGTH: 9
 190 <212> TYPE: PRT
 191 <213> ORGANISM: Homo sapiens
 193 <220> FEATURE:
 194 <223> OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic
 195 myeloid leukemia translocation)
 197 <400> SEQUENCE: 11
 198 Ser Glu Leu Asp Leu Glu Lys Gly Leu

*Please correct this error
in subsequent sequences*

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199      1              5
202 <210> SEQ ID NO: 12
203 <211> LENGTH: 9
204 <212> TYPE: PRT
205 <213> ORGANISM: Homo sapiens
207 <220> FEATURE:
208 <223> OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic
209      myeloid leukemia translocation)
211 <400> SEQUENCE: 12
212 Asp Glu Leu Glu Ala Val Pro Asn Ile
213      1              5
216 <210> SEQ ID NO: 13
217 <211> LENGTH: 9
218 <212> TYPE: PRT
219 <213> ORGANISM: Homo sapiens
221 <220> FEATURE:
222 <223> OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic
223      myeloid leukemia translocation)
225 <400> SEQUENCE: 13
226 Lys Glu Asp Ala Leu Gln Arg Pro Val
227      1              5
230 <210> SEQ ID NO: 14
231 <211> LENGTH: 9
232 <212> TYPE: PRT
233 <213> ORGANISM: Homo sapiens
235 <220> FEATURE:
236 <223> OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic
237      myeloid leukemia translocation)
239 <400> SEQUENCE: 14
240 Glu Asp Ala Leu Gln Arg Pro Val Ala
241      1              5
244 <210> SEQ ID NO: 15
245 <211> LENGTH: 9
246 <212> TYPE: PRT
247 <213> ORGANISM: Homo sapiens
249 <220> FEATURE:
250 <223> OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic
251      myeloid leukemia translocation)
253 <400> SEQUENCE: 15
254 Gly Glu Lys Leu Arg Val Leu Gly Tyr
255      1              5
258 <210> SEQ ID NO: 16
259 <211> LENGTH: 9
260 <212> TYPE: PRT
261 <213> ORGANISM: Homo sapiens
263 <220> FEATURE:
264 <223> OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic
265      myeloid leukemia translocation)
267 <400> SEQUENCE: 16

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RAW SEQUENCE LISTING

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268 Glu Asp Thr Met Glu Val Glu Glu Phe

269 1 5

272 <210> SEQ ID NO: 17

273 <211> LENGTH: 9

274 <212> TYPE: PRT

275 <213> ORGANISM: Homo sapiens

277 <220> FEATURE:

278 <223> OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic
279 myeloid leukemia translocation)

281 <400> SEQUENCE: 17

282 Met Glu Tyr Leu Glu Lys Lys Asn Phe

283 1 5

286 <210> SEQ ID NO: 18

287 <211> LENGTH: 9

288 <212> TYPE: PRT

289 <213> ORGANISM: Homo sapiens

291 <220> FEATURE:

292 <223> OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic
293 myeloid leukemia translocation)

295 <400> SEQUENCE: 18

296 Asn Glu Glu Ala Ala Asp Glu Val Phe

297 1 5

300 <210> SEQ ID NO: 19

301 <211> LENGTH: 9

302 <212> TYPE: PRT

303 <213> ORGANISM: Homo sapiens

305 <220> FEATURE:

306 <223> OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic
307 myeloid leukemia translocation)

309 <400> SEQUENCE: 19

310 Val Asn Gln Glu Arg Phe Arg Met Ile

311 1 5

314 <210> SEQ ID NO: 20

315 <211> LENGTH: 9

316 <212> TYPE: PRT

317 <213> ORGANISM: Homo sapiens

319 <220> FEATURE:

320 <223> OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic
321 myeloid leukemia translocation)

323 <400> SEQUENCE: 20

324 Leu Phe Gln Lys Leu Ala Ser Gln Leu

325 1 5

328 <210> SEQ ID NO: 21

329 <211> LENGTH: 9

330 <212> TYPE: PRT

331 <213> ORGANISM: Homo sapiens

333 <220> FEATURE:

334 <223> OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic
335 myeloid leukemia translocation)

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